

A;Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (c)	
A;Reference number: A56913; MUID:95277838; PMID:7538308	
A;Accession: I49299	
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-656 <RES>	
A;Cross-references: UNIPROT:Q60855; EMBL:025995; NID:9829618; PIDN:AAB60487.1; PID:98296	
C;Genetic:	
A;Gene: RIP	
F;15-293:Domain: protein kinase homology <KIN>	
Query Match 19.5%; Score 115.5 ; DB 2; Length 656;	
Best Local Similarity 34.9%; Prex. No. 0.0039;	
Matches 29; Conservative 22; Mismatches 29; Indels 3; Gaps 3;	
Qy 21 NVICDNGVKDWRRIARQLVKSDTIDSIEDRYPRNN-LITERVRESSLRIWKNTN-KENATVA 78	
Db 573 NPIRNGLGROWNRGCKLGFTESSIDEIDHDYERDGKERVIQMLQRWLMRGTRGTGATVG 632	
Qy 79 HLVGAL-RSCQMVNLADLVQEVO 100	
Db 633 KLAQALHQCCRIDLNLHRLRASQ 655	
RESULT 3	
B35049 ankyrin 1, erythrocyte splice form 3 - human	
N;Alternative names: ankyrin 2.1, erythrocyte; ankyrin-R	
N;Contains: ankyrin 2.2, erythrocyte	
C;Species: Homo sapiens (mam)	
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998	
C;Accession: B35049	
R.Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K	
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990	
A;Title: cDNA sequence for human erythrocyte ankyrin.	
A;Reference number: A35049; PMID:1669649	
A;Accession: B35049	
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-1856 <LAM>	
C;Genetics:	
A;Gene: GDB:ANK1; ANK	
A;Cross-references: GDB:118137; OMIM:182900	
A;Map position: 8p11.2-8p11.2	
C;Superfamily: ankyrin; ankyrin repeat homology	
C;Keywords: alternative splicing	
C;Keywords: ankyrin repeat homology <AN02>	
F;2-1851-1856:Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>	
F;4-47-76:Domain: ankyrin repeat homology <AN02>	
F;77-110:Domain: ankyrin repeat homology <AN02>	
F;110-142:Domain: ankyrin repeat homology <AN02>	
F;143-171:Domain: ankyrin repeat homology <AN02>	
F;172-204:Domain: ankyrin repeat homology <AN02>	
F;205-237:Domain: ankyrin repeat homology <AN02>	
F;238-270:Domain: ankyrin repeat homology <AN02>	
F;271-303:Domain: ankyrin repeat homology <AN02>	
F;304-336:Domain: ankyrin repeat homology <AN02>	
F;331-369:Domain: ankyrin repeat homology <AN02>	
F;370-402:Domain: ankyrin repeat homology <AN1>	
F;403-435:Domain: ankyrin repeat homology <AN12>	
F;436-468:Domain: ankyrin repeat homology <AN13>	
F;469-501:Domain: ankyrin repeat homology <AN14>	
F;502-534:Domain: ankyrin repeat homology <AN15>	
F;535-567:Domain: ankyrin repeat homology <AN16>	
F;568-600:Domain: ankyrin repeat homology <AN17>	
F;601-633:Domain: ankyrin repeat homology <AN18>	
F;634-666:Domain: ankyrin repeat homology <AN19>	
F;667-699:Domain: ankyrin repeat homology <AN20>	
F;700-732:Domain: ankyrin repeat homology <AN21>	
F;733-765:Domain: ankyrin repeat homology <AN22>	
F;766-798:Domain: ankyrin repeat homology <AN23>	
Query Match 19.3%; Score 114.5 ; DB 2; Length 1856;	

RESULT 5

STHUK
ankyrin 1, erythrocyte splice form 1 - human
N; Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N; Contains: ankyrin 2.2
C; Species: Homo sapiens (man)
C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C; Accession: S08275; A33219; P2220; A35443
R; Lux, S.E.; John, K.M.; Bennett, V.
Nature 344, 36-42, 1990
A; Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure
A; Reference number: S08275; MUID:90158830; PMID:2137557
A; Accession: S08275
A; Molecule type: protein
A; Residues: 1-1861 <LNU>
A; Cross-references: UNIPROT:PI16157; EMBL:X16609; NID:928701; PIDN:CAA34610.1; PID:928702
A; Accession: A33219
A; Molecule type: protein
A; Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30, 733-749, 'A', 751-753, 828-833, 'X', 835-855, 'X'
X'1367-1383-1427;1601-1630;1686-1698; D1700;1763-1772 <LUK>
A; Note: 945-Arg and 1392-Thr were also found
R; Hermann, J.; Barel, M.; Prade, R.
Biochem Biophys Res Commun. 204, 453-460, 1994
A; Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
A; Reference number: P2220; MUID:95071348; PMID:7526850
A; Accession: PC2220
A; Molecule type: protein
A; Residues: 910-329 <BER>
R; Davis, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
A; Title: Mapping binding sites of human erythrocyte ankyrin for the anion exchanger
A; Reference number: A55443; MUID:90285190; PMID:2141335
A; Accession: A35443
A; Molecule type: protein
A; Residues: 'X', 5, 'X', 7-12; 403-417, 'X', 419-422, 'H', 424, 'IQ', 797-800, 'L', 802-814; 862-863,
C; Genetics:
A; Gene: GDB:ANK1; ANK
A; Cross-references: GDB:118737; OMIM:182900
A; Map position: 8p1.2-8p11.2
C; Superfamily: ankyrin repeat homology
C; Keywords: alternative splicing; phosphoprotein
P2-1881/Product: ankyrin 1, erythrocyte Form 1 #status predicted <MAT1>
P2-1881/Region: ankyrin 2.1, erythrocyte #status predicted <MAT2>
P2-8274/Domain: 89K #status predicted <D011>
P2-8274/Region: anion exchange protein binding
P44-45/Domain: ankyrin repeat homology <AN01>
P77-109/Domain: ankyrin repeat homology <AN02>
P110-142/Domain: ankyrin repeat homology <AN03>
P143-171/Domain: ankyrin repeat homology <AN04>
P172-204/Domain: ankyrin repeat homology <AN05>
P205-237/Domain: ankyrin repeat homology <AN06>
P271-303/Domain: ankyrin repeat homology <AN07>
P303-336/Domain: ankyrin repeat homology <AN08>
P370-402/Domain: ankyrin repeat homology <AN09>
P404-435/Domain: ankyrin repeat homology <AN11>
P436-468/Domain: ankyrin repeat homology <AN12>
P469-501/Domain: ankyrin repeat homology <AN13>
P502-534/Domain: ankyrin repeat homology <AN15>
P515-567/Domain: ankyrin repeat homology <AN17>
P568-600/Domain: ankyrin repeat homology <AN18>
P601-633/Domain: ankyrin repeat homology <AN19>
P667-699/Domain: ankyrin repeat homology <AN20>
P700-732/Domain: ankyrin repeat homology <AN21>
P766-798/Domain: ankyrin repeat homology <AN22>
P828-1382/Region: spectrin predicted <DOM2>
P1383-1881/Domain: 55K #status predicted <DOM3>

RESULT 6

S37771
ankyrin, erythrocyte - mouse
C; Species: Mus musculus (house mouse)
C; Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C; Accession: S37771
R; Birkenmaier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.B.
J. Biol. Chem. 268, 9533-9540, 1993
A; Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found in
A; Reference number: S37771; MUID:93252825; PMID:8486643
A; Accession: S37771
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1848 <BIR>
A; Cross-references: UNIPROT:Q61302; EMBL:X69063; NID:9311816; PIDN:CAA48801.1; PID:9311
C; Keywords: ankyrin, ankyrin repeat homology
C; Keywords: alternative splicing
F; 81-113/Domain: ankyrin repeat homology <AN02>
F; 114-146/Domain: ankyrin repeat homology <AN03>
F; 147-175/Domain: ankyrin repeat homology <AN04>
F; 176-208/Domain: ankyrin repeat homology <AN05>
F; 209-241/Domain: ankyrin repeat homology <AN06>
F; 242-274/Domain: ankyrin repeat homology <AN07>
F; 275-307/Domain: ankyrin repeat homology <AN08>
F; 308-340/Domain: ankyrin repeat homology <AN09>
F; 341-373/Domain: ankyrin repeat homology <AN10>
F; 374-406/Domain: ankyrin repeat homology <AN11>
F; 407-439/Domain: ankyrin repeat homology <AN12>
F; 440-472/Domain: ankyrin repeat homology <AN13>
F; 473-505/Domain: ankyrin repeat homology <AN14>
F; 506-538/Domain: ankyrin repeat homology <AN15>
F; 539-571/Domain: ankyrin repeat homology <AN16>
F; 572-604/Domain: ankyrin repeat homology <AN17>
F; 605-637/Domain: ankyrin repeat homology <AN18>
F; 638-670/Domain: ankyrin repeat homology <AN19>
F; 671-703/Domain: ankyrin repeat homology <AN20>
F; 704-736/Domain: ankyrin repeat homology <AN21>
F; 737-769/Domain: ankyrin repeat homology <AN22>
F; 770-802/Domain: ankyrin repeat homology <AN23>

Query Match 19.3%; Score 114.5; DB 1; Length 1881;
Best Local Similarity 28.1%; Pred. No. 0.016; Mismatches 26; Indels 7; Gaps 2;

Query Match 19.0%; Score 112.5; DB 2; Length 1848;
Best Local Similarity 29.0%; Pred. No. 0.024; Mismatches 27; Indels 7; Gaps 2;

Query Match 22.0%; Score 114.5; DB 3; Length 1480;
Best Local Similarity 29.0%; Pred. No. 0.024; Mismatches 37; Indels 7; Gaps 2;

Query Match 22.0%; Score 114.5; DB 4; Length 1520;
Best Local Similarity 29.0%; Pred. No. 0.024; Mismatches 37; Indels 7; Gaps 2;

RESULT 7

149502
ankyrin - mouse
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: I49502

A;Gene: CESP:unc-44
A;Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979
C;Superfamily: ankyrin; ankyrin repeat homology <AN04>
P;164-192/Domain: ankyrin repeat homology <AN1>
P;358-390/Domain: ankyrin repeat homology <AN11>
P;391-423/Domain: ankyrin repeat homology <AN11>

Query Match Score 1.03; DB 2; Length 2039;
Best Local Similarity 31.9%; Pred. No. 0.21; Matches 30; Conservative 15; Mismatches 41; Indels 8; Gaps 3;

Qy 23 ICDNVGKDWRRQLAROLKVSDTIDSTEDRYPRNLTERVRESLRWKNTENATAVHLVG 82
Db 1504 VLRKGIGADPWRGLRALEYPHRDIQHTRONYP --GQBKNLKIWIHLKEDANQDNLDQ 1560

Qy 83 ALRSQCMNLVADLYQEYQ/QARD -LQNNSGAMP 114
Db 1561 ALRQIGRDL --DIVRSTAYGEPDALNYSQADSP 1591

RESULT 10
S37431 neuronal long splice form - human
N:Alternative names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid
N:Contains: ankyrin 2, short form
R:Chan, W.

Submitted to the EMBL Data Library, September 1993
A:Reference number: S37431
A:Accession: S37431
A:Status: preliminary
A:Molecule type: mRNA
A:Cross-references: EMBL:1-3924 <CIR>
A:Residues: 1-3924
A:Cross-references: UNIPROT:Q01484; EMBL:226634; NID:9406287; PID:CAA81387.1; PMID:g4062
R:Otto, B.; Kunitomo, M.; McLaughlin, T.; Bennett, V.
J:Cell Biol. 114, 241-253, 1991
A:Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
A:Reference number: A39643; MUID:91302466; PMID:1830053
A:Accession: A39643
A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: GB:X56957
A:Residues: 1-2077 <OTI>
A:Cross-references: BJ9643
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1443,3585-3924 <OTI>
A:Cross-references: EMBL:X55958
R:Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
Genomics 10, 858-866, 1991
A:Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A:Reference number: A40334; MUID:92009921; PMID:1833308
A:Accession: A40334
A:Molecule type: DNA
A:Residues: 463-474, 'PR', 477-495 <TSE>
A:Cross-references: GB:B37123; NID:9178647; PID:AAA62828.1; PMID:g1786488
R:Chan, W.; Kordeli, E.; Bennett, V.
J:Cell Biol. 123, 1463-1473, 1993
A:Title: 440-kD ankyrins: structure of the major developmentally regulated domain and se
A:Reference number: A49462; MUID:94075409; PMID:8253844
A:Accession: A49462
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-3924 <RES>
A:Cross-references: EMBL:Z26634; NID:9406287; PID:CAA81387.1; PMID:g406288
C:Genetics:
A:Gene: GDB:Ank2
A:Cross-references: GDB:127607; OMIM:106410
A:Map position: 4q23-4q27
C:Superfamily: ankyrin repeat homology
C:Keywords: alternative splicing

F;2-1924/Product: ankyrin 2, long form #status Predicted <MAT>
F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <NA2>
F;63-95/Domain: ankyrin repeat homology <AN02>
F;96-128/Domain: ankyrin repeat homology <AN03>
F;129-161/Domain: ankyrin repeat homology <AN04>
F;162-190/Domain: ankyrin repeat homology <AN05>
F;191-223/Domain: ankyrin repeat homology <AN06>
F;232-264/Domain: ankyrin repeat homology <AN07>
F;265-297/Domain: ankyrin repeat homology <AN08>
F;298-330/Domain: ankyrin repeat homology <AN09>
F;331-363/Domain: ankyrin repeat homology <AN10>
F;364-396/Domain: ankyrin repeat homology <AN11>
F;397-429/Domain: ankyrin repeat homology <AN11>
F;430-462/Domain: ankyrin repeat homology <AN12>
F;463-495/Domain: ankyrin repeat homology <AN13>
F;496-528/Domain: ankyrin repeat homology <AN14>
F;529-561/Domain: ankyrin repeat homology <AN15>
F;562-594/Domain: ankyrin repeat homology <AN16>
F;595-627/Domain: ankyrin repeat homology <AN17>
F;628-660/Domain: ankyrin repeat homology <AN18>
F;661-693/Domain: ankyrin repeat homology <AN19>
F;694-726/Domain: ankyrin repeat homology <AN20>
F;727-759/Domain: ankyrin repeat homology <AN21>
F;760-792/Domain: ankyrin repeat homology <AN22>
F;793-825/Domain: ankyrin repeat homology <AN23>

Query Match Score 16.3%; DB 2; Length 3924;
Best Local Similarity 24.3%; Pred. No. 1.8;
Matches 25; Conservative 21; Mismatches 42; Indels 15; Gaps 1;

Qy 23 ICDNVGKDWRRQLAROLKVSDTIXDSTDERTDRYPRNLTERVRESLRWKNTENATAVHLVG 82
Db 3543 IADHLGFSWTELARBLDETEQHQIQRRIENPNLSQDSQYLKWIWERDGRHATDTNLVE 3602

Qy 83 ALRSQCMNLVADLYQEYQ/QARD -----EVOQARDLQNRSQ 110
Db 3603 CLTKINRMIVHLMETNEPLQERISHSYAEEQTTLDHSSEG 3645

RESULT 11
JC2395
P: antigen precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Accession: JC2395; PC2246
C:Cross-references: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 66-674, 1994
A:Title: A variant mRNA species encoding a truncated from of Pas antigen in the rat liver
A:Reference number: JCC2395; MUID:94128114; PMID:7507668
A:Accession: JC2395
A:Molecule type: mRNA
A:Residues: 1-324 <KIM>
A:Cross-references: UNIPROT:Q63199; DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PMID:d100
A:Experimental source: thymus
A:Accession: PC2246
A:Molecule type: mRNA
A:Residues: 1-62, RFT, <K12>
A:Cross-references: DDBJ:D6113; NID:9468488; PIDN:BAA05109.1; PID:9468488
A:Experimental source: liver
C:Genetics:
A:Introns: 62/1
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: transmembrane protein
F;21/Domain: signal sequence #status predicted <STG>
F;22-32/Product: Pas antigen #status predicted <MAT>
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-128/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TM>

Query Match Score 15.7%; DB 2; Length 324;
Best Local Similarity 28.2%; Pred. No. 0.24;
Matches 22; Conservative 16; Mismatches 32; Indels 8; Gaps 2;

Qy 23 ICDNVGKDWRLLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTKEKENATAVAHLV 82
 Db 231 ICDA---KKPARQKIPKESKIDEHNSFQDAAEQKTFOLLQCWYQSGKTGACQALIQ 285

Qy 83 ALRSQMMVLADLVQEYQ 100
 Db 286 GLRKANR---CDIAEEIQ 300

RESULT 12

T42714 ankyrin 3, splice form 2 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T42714
 R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, L.J. Cell Biol. 130, 313-330, 1995
 A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.
 A;Reference number: Z22237; MUID:95340633; PMID:7615634
 A;Accession: T42714
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1765 <PRT>
 A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:9710548; PID:9710551; PIDN:AAB01605
 A;Experimental source: strain C57BL/6J; kidney
 C;Keywords: alternative splicing
 A;Gene: Ank3
 A;Map Position: 10
 A;Introns: 1587/1
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing

Query Match Score 86; DB 2; Length 1765;
 Best Local Similarity 29.0%; Pred. No. 74;
 Matches 27; Conservative 18; Mismatches 44; Indels 4; Gaps 3;

Qy 22 VICDNVGKDWRLLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTKEKENATAVAHLV 81
 Db 1484 IVADHGLGSWTELARELNFSVDEINQIRVENPNSLISQEFMLLKWKVTRDGKNATTDA 1543

Qy 82 GALRSQMMVLADLVQEYQ-QARDLQNRSGAMS 113
 Db 1544 SVL--TKINRI-DIVTLELEGPIFYGNISGTRS 1573

RESULT 13

T42715 ankyrin 3, splice form 3 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T42715
 R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, L.J. Cell Biol. 130, 313-330, 1995
 A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.
 A;Reference number: Z22237; MUID:95340633; PMID:7615634
 A;Accession: T42715
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1940 <PRT>
 A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:9710548; PID:9710549; PIDN:AAB01604
 A;Experimental source: strain C57BL/6J; kidney
 C;Keywords: alternative splicing

Query Match Score 86; DB 2; Length 1940;
 Best Local Similarity 29.0%; Pred. No. 82;
 Matches 27; Conservative 18; Mismatches 44; Indels 4; Gaps 3;

Qy 22 VICDNVGKDWRLLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTKEKENATAVAHLV 81
 Db 1463 IVADHGLGSWTELARELNFSVDEINQIRVENPNSLISQEFMLLKWKVTRDGKNATTDA 1522

Qy 82 GALRSQMMVLADLVQEYQ-QARDLQNRSGAMS 113
 Db 1523 SVL--TKINRI-DIVTLELEGPIFYGNISGTRS 1552

RESULT 14

T42713 ankyrin 3, splice form 1 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T42713
 R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, L.J. Cell Biol. 130, 313-330, 1995
 A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.
 A;Reference number: Z22237; MUID:95340633; PMID:7615634
 A;Accession: T42713
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1943 <PRT>
 A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:9710548; PID:9710550; PIDN:AAB01606
 A;Experimental source: strain C57BL/6J; kidney
 C;Keywords: alternative splicing
 C;Genetics:
 A;Gene: Ank3
 A;Map position: 10
 A;Introns: 855/1
 C;Function:
 A;Description: supposed to play an important role in the polarized distribution of many A;Note: major kidney ankyrin
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing

Query Match Score 86; DB 2; Length 1943;
 Best Local Similarity 29.0%; Pred. No. 8.3;
 Matches 27; Conservative 18; Mismatches 44; Indels 4; Gaps 3;

Qy 22 VICDNVGKDWRLLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTKEKENATAVAHLV 81
 Db 1466 IVADHGLGSWTELARELNFSVDEINQIRVENPNSLISQEFMLLKWKVTRDGKNATTDA 1525

Qy 82 GALRSQMMVLADLVQEYQ-QARDLQNRSGAMS 113
 Db 1526 SVL--TKINRI-DIVTLELEGPIFYGNISGTRS 1555

RESULT 15

A45627 myosin heavy chain [similarity] - nematode (Brugia malayi)
 C;Species: Brugia malayi
 C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A45627; B45526
 R;Werner, C.; Rajan, T.V.
 Mol. Biochem. Parasitol. 50, 261-268, 1992
 A;Title: Characterization of a myosin heavy chain gene from Brugia malayi.
 A;Reference number: A45627
 A;Accession: A45627
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1957 <PRT>
 A;Cross-references: UNIPROT:Q04009; GB:M74000; NID:9156086; PIDN:AAA73080.1; PMID:g156087
 A;Note: sequence extracted from NCBI backbone (NCBIN:83576, NCBI:83578)
 R;Werner, C.; Higashi, G.I.; Yates, J.A.; Rajan, T.V.
 Mol. Biochem. Parasitol. 35, 209-218, 1989
 A;Title: Differential recognition of two cloned Brugia malayi antigens by antibody class
 A;Reference number: A45526
 A;Accession: B45526
 A;Status: preliminary
 A;Molecule type: DNA

A) Residues: 'R',1491-1556 <WB2>

A) Cross references: GB-J04645

A) Note: the authors translated the codon TTC for residue 1540 as Lys

C) Superfamily: myosin heavy chain; myosin motor domain homology

C) Keywords: ATP; nucleotide binding; P-loop

P:89-773/Domain: myosin motor domain homology <MMOT>

P:179-186/Region: nucleotide-binding motif A (P-loop)

Query Match 14.5%; Score 86; DB 2; Length 1957;

Best Local Similarity 28.0%; Pred. No. 8.8; Matches 26; Conservative 23; Mismatches 32; Indels 12; Gaps 4;

Qy 25 DNVGKDWRRIARQLKVSITKIDSIE--DRYPRNLTVERRESURIWNTKEENATVAHLV 81

Db 1053 NEIEKQKRKIGGELKVADQENMEEITERQRHEIESNLKKESEQAIIITRLLEERQ---DIL 1108

Qy 82 GALRSQO--MNLVADLYQEVQARDLQNRSGA 111

Db 1109 GSLKTCQRTIQNRISELEEBLENER-QSRSKA 1139

Search completed: February 11, 2005, 16:41:35

Job time : 67 secs

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